SEQUENCE LISTING

<110> NEWELL, MARTHA K

<120> METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE

<130> V0139.70017US00

<140> US 10/616,865
<141> 2003-07-09

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<151> 1999-03-27

<150> US 60/082,250
<151> 1998-04-17

<150> US 60/101,580
<151> 1998-09-24

<150> US 60/094,519
<151> 1998-07-29

<160> 13

<170> PatentIn version 3.2

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gtgaaactaa atccacaacc tttggagacc caggaacacc ctccaatctc tgtgtgtttt 180

gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcagc cctgcctgtt 240

ttgcacctgg gaagtgccct ggtcttactt gggtccaaat tgttggcttt cacttttgac 300

cctaagcatc tgaagccatg ggccacacac ggaggcaggg aacatcacca tccaagtgtc 360

catacctcaa tttctttcag ctcttggtgc tggctggtct ttctcacttc tgttcaggtg 420

ttatccacgt gaccaaggaa gtgaaagaag tggcaacgct gtcctgtggt cacaatgttt 480

ctgttgaaga gctggcacaa actcgcatct actggcaaaa ggagaagaaa atggtgctga 540

ctatgatgtc tggggacatg aatatatggc ccgagtacaa gaaccggacc atctttgata 600

tcactaataa cctctccatt gtgatcctgg ctctgcgccc atctgacgag ggcacatacg 660

agtgtgttgt tctgaagtat gaaaaagacg ctttcaagcg ggaacacctg gctgaagtga 720

cgttatcagt caaagctgac ttccctacac ctagtatatc tgactttgaa attccaactt 780

ctaatattag aaggataatt tgctcaacct ctggaggttt tccagagcct cacctctcct 840

ggttggaaaa tggagaagaa ttaaatgcca tcaacacaac agtttcccaa gatcctgaaa 900

ctgagctcta tgctgttagc agcaaactgg atttcaatat gacaaccaac cacagcttca 960

tgtgtctcat caagtatgga catttaagag tgaatcagac cttcaactgg aatacaacca 1020

agcaagagca ttttcctgat aacctgctcc catcctgggc cattacctta atctcagtaa 1080

atggaatttt tgtgatatgc tgcctgacct actgctttgc cccaagatgc agagagagaa 1140

ggaggaatga gagattgaga agggaaagtg tacgccctgt ataacagtgt ccgcagaagc 1200

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<210> 2
<211> 288
<212> PRT
<213> Homo sapiens

<400> 2

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Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

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Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
            180                 185                 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
        195                 200                 205

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
    210                 215                 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225                 230                 235                 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
                245                 250                 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
            260                 265                 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
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cagtggacag gcatttgtga cagcactatg ggactgagta acattctctt tgtgatggcc    180

ttcctgctct ctggtgctgc tcctctgaag attcaagctt atttcaatga gactgcagac    240

ctgccatgcc aatttgcaaa ctctcaaaac caaagcctga gtgagctagt agtattttgg    300

caggaccagg aaaacttggt tctgaatgag gtatacttag gcaaagagaa atttgacagt    360

gttcattcca agtatatggg ccgcacaagt tttgattcgg acagttggac cctgagactt    420

cacaatcttc agatcaagga caagggcttg tatcaatgta tcatccatca caaaaagccc    480

acaggaatga ttcgcatcca ccagatgaat tctgaactgt cagtgcttgc taacttcagt    540

caacctgaaa tagtaccaat ttctaatata acagaaaatg tgtacataaa tttgacctgc    600

tcatctatac acggttaccc agaacctaag aagatgagtg ttttgctaag aaccaagaat    660

tcaactatcg agtatgatgg tattatgcag aaatctcaag ataatgtcac agaactgtac    720

gacgtttcca tcagcttgtc tgtttcattc cctgatgtta cgagcaatat gaccatcttc    780

tgtattctgg aaactgacaa gacgcggctt ttatcttcac ctttctctat agagcttgag    840

gaccctcagc ctccccaga ccacattcct tggattacag ctgtacttcc aacagttatt    900

atatgtgtga tggttttctg tctaattcta tggaaatgga agaagaagaa gcggcctcgc    960

aactcttata aatgtggaac caacacaatg gagagggaag agagtgaaca gaccaagaaa   1020
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agagaaaaaa tccatatacc tgaaagatct gatgaagccc agcgtgtttt taaaagttcg 1080

aagacatctt catgcgacaa aagtgataca tgtttttaat taaagagtaa agcccataca 1140

agtattcatt ttttctaccc tttcctttgt aagttcctgg gcaacctttt tgatttcttc 1200

cagaaggcaa aaagacatta ccatgagtaa taaggggget ccaggactcc ctctaagtgg 1260

aatagcctcc ctgtaactcc agctctgctc cgtatgccaa gaggagactt taattctctt 1320

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ctggaaataa aatttaggac caataaaaaa aaaaaaaaaa aaaa 1424

<210> 4
<211> 323
<212> PRT
<213> Homo sapiens

<400> 4

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1 5 10 15

Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
20 25 30

Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
35 40 45

Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50 55 60

Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65 70 75 80

Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
85 90 95

Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
100 105 110

Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
115 120 125

Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
130 135 140

Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
145 150 155 160

Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
165 170 175

Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
180 185 190

Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
195 200 205

```
Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
    210                 215                 220

Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
225                 230                 235                 240

Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
                245                 250                 255

Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn
            260                 265                 270

Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
        275                 280                 285

Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
    290                 295                 300

Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp
305                 310                 315                 320

Thr Cys Phe
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<210> 5
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<212> DNA
<213> Homo sapiens

<400> 5

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ctccaggtcc aaggtgaatg cccgacgtcc agtgttatta ggtataaagg tgtcctggga    180

acaatcaccg ctgtggtaaa aacagaaggg cggatgaaac tctacagcgg gctgcctgcg    240

gggcttcagc ggcaaatcag ctccgcctct ctcaggatcg gcctctacga cacggtccag    300

gagttcctca ccgcagggaa agaaacagca cctagtttag gaagcaagat tttagctggt    360

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cttcaagcac agagccatct ccacggaatc aaacctcgct acacggggac ttataatgcg    480

tacagaataa tagcaacaac cgaaggcttg acgggtcttt ggaaagggac tactcccaat    540

ctgatgagaa gtgtcatcat caattgtaca gagctagtaa catatgatct aatgaaggag    600

gcctttgtga aaaacaacat attagcagat gacgtcccct gccacttggt gtcggctctt    660

atcgctggat tttgcgcaac agctatgtcc tccccggtgg atgtagtaaa aaccagattt    720

attaattctc caccaggaca gtacaaaagt gtgcccaact gtgcaatgaa agtgttcact    780

aacgaaggac caacggcttt cttcaagggg ttggtacctt ccttcttgcg acttggatcc    840

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cagactatgg actgtgccac ataa                                          924
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<210> 6
<211> 307
<212> PRT
<213> Homo sapiens

<400> 6

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Met Gly Gly Leu Thr Ala Ser Asp Val His Pro Thr Leu Gly Val Gln
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Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
            20                  25                  30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
        35                  40                  45

Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
    50                  55                  60

Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
65                  70                  75                  80

Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr
                85                  90                  95

Asp Thr Val Gln Glu Phe Leu Thr Ala Gly Lys Glu Thr Ala Pro Ser
            100                 105                 110

Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val
        115                 120                 125

Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln
    130                 135                 140

Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala
145                 150                 155                 160

Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly
                165                 170                 175

Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu
            180                 185                 190

Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu
        195                 200                 205

Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe
    210                 215                 220

Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg Phe
225                 230                 235                 240

Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met
                245                 250                 255

Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val
            260                 265                 270

Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys
        275                 280                 285
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Cys Ala Thr
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<210> 7
<211> 1105
<212> DNA
<213> Homo sapiens

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tactgccact gtgaagtttc ttggggctgg cacagctgcc tgcatcgcag atctcatcac 180

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gcgcgctaca gccagcgccc agtaccgcgg tgtgatgggc accattctga ccatggtgcg 300

tactgagggc ccccgaagcc tctacaatgg gctggttgcc ggcctgcagc gccaaatgag 360

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<210> 8
<211> 309
<212> PRT
<213> Homo sapiens

<400> 8

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Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
            20                  25                  30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
        35                  40                  45

Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
    50                  55                  60

Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
65                  70                  75                  80

Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
                85                  90                  95

Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
            100                 105                 110

His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
        115                 120                 125

Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
    130                 135                 140

Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
145                 150                 155                 160

Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
                165                 170                 175

Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
            180                 185                 190

Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
        195                 200                 205

Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
    210                 215                 220

Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
225                 230                 235                 240

Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
                245                 250                 255

Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
            260                 265                 270

Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
        275                 280                 285

Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
    290                 295                 300

Arg Glu Ala Pro Phe
305
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<211> 1132
<212> DNA
<213> Homo sapiens

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ctcgggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc 660

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<210> 10
<211> 275
<212> PRT
<213> Homo sapiens

<400> 10

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Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe
20 25 30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
35 40 45

Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
50 55 60

Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly
65 70 75 80

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Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile
                85                  90                  95

Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
            100                 105                 110

Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala
        115                 120                 125

Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
    130                 135                 140

Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser
145                 150                 155                 160

Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg
                165                 170                 175

Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val
            180                 185                 190

Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu
        195                 200                 205

Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala
    210                 215                 220

Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val
225                 230                 235                 240

Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro
                245                 250                 255

Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe
            260                 265                 270

Tyr Lys Gly
        275
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<210> 11
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 11

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gggaaattgg gcaatgaatc agtgacattc tacctccaga atttgtatgt taaccaaaca    420

gatatttact tctgcaaaat tgaagttatg tatcctcctc cttacctaga caatgagaag    480
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tgactgagaa gttagggtag aaaacaaaaa gggagtggat tctgggagcc tcttcccttt 1080

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ggttaaacgg ggtaagttag agtaggggga gggataggaa gacatattta aaaaccatta 1260

aaacactgtc tcccactcat gaaatgagcc acgtagttcc tatttaatgc tgttttcctt 1320

tagtttagaa atacatagac attgtctttt atgaattctg atcatattta gtcattttga 1380

ccaaatgagg gatttggtca aatgagggat tccctcaaag caatatcagg taaaccaagt 1440

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gaataaaata gttc 1514

<210> 12
<211> 220
<212> PRT
<213> Homo sapiens

<400> 12

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95

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Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130                 135                 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145                 150                 155                 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165                 170                 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            180                 185                 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        195                 200                 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    210                 215                 220


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Arg His Arg Ser Gln Lys Gly Pro
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